RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/811,080_

Source: _____

Date Processed by STIC: _____

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IFWO

RAW SEQUENCE LISTING   DATE: 10/18/2004
PATENT APPLICATION: US/10/811,080   TIME: 10:03:39

        Input Set : N:\Crf3\RULE60\10811080.raw.txt
        Output Set: N:\CRF4\10182004\J811080.raw

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 1 <110> APPLICANT: Gerritsen, Mary E.
 2         Goddard, Audrey
 3         Grimaldi, J. Christopher
 4         Mehraban, Fuad
 5 <120> TITLE OF INVENTION: NOVEL POLYPEPTIDES, THEIR NUCLEIC ACIDS, AND METHODS
 6         FOR THEIR USE IN ANGIOGENESIS AND VASCULARIZATION
 7 <130> FILE REFERENCE: P1776R2US
 8 <140> CURRENT APPLICATION NUMBER: US/10/811,080
 9 <141> CURRENT FILING DATE: 2004-03-26
10 <150> PRIOR APPLICATION NUMBER: US/09/684,458
11 <151> PRIOR FILING DATE: 2000-10-05
12 <150> PRIOR APPLICATION NUMBER: US 60/158,587
13 <151> PRIOR FILING DATE: 1999-10-07
14 <150> PRIOR APPLICATION NUMBER: US 60/162,611
15 <151> PRIOR FILING DATE: 1999-10-28
16 <160> NUMBER OF SEQ ID NOS: 29
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2891
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
22 <400> SEQUENCE: 1
23       ggcgggagtc ggcgcctcgg gttcctacct cgcgtcccta ggcggcggcg 50
24       gccgggcgtc ccggg    atg gcc ttc atg gag aag ccg cca 89
25                          Met Ala Phe Met Glu Lys Pro Pro
26                            1               5
27       gcc ggc aag gtg ctg ctg gac gac acg gtg ccg ctg aca 128
28       Ala Gly Lys Val Leu Leu Asp Asp Thr Val Pro Leu Thr
29            10              15                  20
30       gca gcc atc gag gcg agc cag agc ctg cag tcc cac acg 167
31       Ala Ala Ile Glu Ala Ser Gln Ser Leu Gln Ser His Thr
32                25                  30
33       gaa tat att att cga gtg caa aga gga att tct gtg gaa 206
34       Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser Val Glu
35        35                  40                  45
36       aac agc tgg cag att gtt aga aga tac agt gac ttt gat 245
37       Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
38                50                  55                  60
39       ttg ctt aac aac agc tta cag att gca ggc cta agt cta 284
40       Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu
41                        65                  70
42       cct ctt cct ccc aaa aaa ttg att ggt aac atg gat cgt 323
43       Pro Leu Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg
44            75                  80                  85
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45      gaa ttc ata gct gaa agg cag aaa ggt ctt cag aac tat 362
46      Glu Phe Ile Ala Glu Arg Gln Lys Gly Leu Gln Asn Tyr
47                      90                  95
48      ctc aac gtg atc aca aca aat cat atc ttg tct aat tgt 401
49      Leu Asn Val Ile Thr Thr Asn His Ile Leu Ser Asn Cys
50      100                 105                 110
51      gag ctg gtt aag aag ttt tta gat cca aac aac tat tcc 440
52      Glu Leu Val Lys Lys Phe Leu Asp Pro Asn Asn Tyr Ser
53                  115                 120             125
54      gca aac tat act gag att gcc ttg caa cag gtt tcc atg 479
55      Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln Val Ser Met
56                      130                 135
57      ttc ttc cga tca gaa cca aag tgg gag gtg gtg gaa cct 518
58      Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu Pro
59          140                 145                 150
60      ttg aaa gac ata ggt tgg aga ata agg aag aaa tat ttc 557
61      Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe
62                  155                 160
63      ttg atg aag att aaa aat cag cca aag gaa cgg cta gtg 596
64      Leu Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val
65      165                 170                 175
66      tta agc tgg gct gac ctt ggc cca gac aag tat ttg tca 635
67      Leu Ser Trp Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser
68                  180                 185             190
69      gat aaa gat ttt cag tgt cta atc aaa ctt ctg cct tct 674
70      Asp Lys Asp Phe Gln Cys Leu Ile Lys Leu Leu Pro Ser
71                      195                 200
72      tgt ttg cac cct tac atc tat cgg gtt acc ttt gcc aca 713
73      Cys Leu His Pro Tyr Ile Tyr Arg Val Thr Phe Ala Thr
74          205                 210                 215
75      gct aat gaa tcc tca gcg ttg cta att agg atg ttt aac 752
76      Ala Asn Glu Ser Ser Ala Leu Leu Ile Arg Met Phe Asn
77                  220                 225
78      gaa aag gga aca ttg aag gat ctg atc tac aag gca aaa 791
79      Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys Ala Lys
80      230                 235                 240
81      cca aaa gac cca ttt cta aag aag tac tgc aac cct aag 830
82      Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
83                  245                 250             255
84      aag att cag ggc ctg gaa ctc cag caa ata aaa aca tat 869
85      Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr
86                      260                 265
87      gga cgg caa ata tta gag gta ctg aag ttt ctt cat gac 908
88      Gly Arg Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp
89          270                 275                 280
90      aag gga ttc cct tat ggg cat ctt cac gcc tcc aat gtg 947
91      Lys Gly Phe Pro Tyr Gly His Leu His Ala Ser Asn Val
92                  285                 290
93      atg ctc gat ggg gac act tgt cgg ctg ctg gac ctt gag 986
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94      Met Leu Asp Gly Asp Thr Cys Arg Leu Leu Asp Leu Glu
95      295                 300                 305
96      aat tcc tta ttg ggc ctg cct tcc ttc tac cga tct tat 1025
97      Asn Ser Leu Leu Gly Leu Pro Ser Phe Tyr Arg Ser Tyr
98              310                 315             .   320
99      ttt tca caa ttc agg aaa atc aat aca ttg gaa agt gtg 1064
100     Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu Glu Ser Val
101                         325                 330
102     gat gtc cac tgc ttt ggc cac tta ctg tat gaa atg act 1103
103     Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met Thr
104             335                 .   340                 345
105     tat gga cga ccg cca gac tcg gtg cct gtg gac tcc ttc 1142
106     Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe
107                         350                 355
108     cct cct gcc ccg tcc atg gct gtg gtg gcc gtg ttg gag 1181
109     Pro Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu
110     360                 365                 370
111     tct acg ctg tct tgt gaa gcc tgt aaa aat ggc atg cct 1220
112     Ser Thr Leu Ser Cys Glu Ala Cys Lys Asn Gly Met Pro
113             375                 380                 385
114     acc atc tcc cgg ctc tta cag atg cca tta ttc agc gat 1259
115     Thr Ile Ser Arg Leu Leu Gln Met Pro Leu Phe Ser Asp
116                         390                 395
117     gtt tta cta acc act tct gaa aaa cca cag ttt aag atc 1298
118     Val Leu Leu Thr Thr Ser Glu Lys Pro Gln Phe Lys Ile
119             400                 405                 410
120     cct aca aag tta aaa gag gca ttg aga att gcc aaa gaa 1337
121     Pro Thr Lys Leu Lys Glu Ala Leu Arg Ile Ala Lys Glu
122                 415                 420
123     tgt ata gag aag aga cta att gag gaa cag aaa cag att 1376
124     Cys Ile Glu Lys Arg Leu Ile Glu Glu Gln Lys Gln Ile
125     425                 430                 435
126     cac cag cat cga aga ctg aca aga gct cag tcc cac cat 1415
127     His Gln His Arg Arg Leu Thr Arg Ala Gln Ser His His
128             440                 445                 450
129     gga tct gag gag gaa aga aaa aaa aga aag att tta gct 1454
130     Gly Ser Glu Glu Glu Arg Lys Lys Arg Lys Ile Leu Ala
131                 455                 460
132     cga aag aag tca aaa cga tct gct ctt gaa aat agt gaa 1493
133     Arg Lys Lys Ser Lys Arg Ser Ala Leu Glu Asn Ser Glu
134             465                 470                 475
135     gag cat tca gcg agg tac agc aac tcc aat aat tca gga 1532
136     Glu His Ser Ala Arg Tyr Ser Asn Ser Asn Asn Ser Gly
137                 480                 485
138     tct ggg gcc agc tca cct ctc acg tcc ccg tca tcg cca 1571
139     Ser Gly Ala Ser Ser Pro Leu Thr Ser Pro Ser Ser Pro
140     490                 495                 500
141     act cca ccc tct aca tca ggg ata tct gca tta cct cca 1610
142     Thr Pro Pro Ser Thr Ser Gly Ile Ser Ala Leu Pro Pro
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143            505               510               515
144     cct cct cca cct cca cca cca cca gca gct ccc ttg cct 1649
145     Pro Pro Pro Pro Pro Pro Pro Pro Ala Ala Pro Leu Pro
146                520               525
147     cct gcg agc acc gag gta cct gcc cag ctc tcg tct cag 1688
148     Pro Ala Ser Thr Glu Val Pro Ala Gln Leu Ser Ser Gln
149      530               535               540
150     gct gtg aat ggc atg agc cga ggg gcc ttg ctc agc tcc 1727
151     Ala Val Asn Gly Met Ser Arg Gly Ala Leu Leu Ser Ser
152                545               550
153     atc cag aat ttc caa aaa gga act ttg agg aaa gcc aaa 1766
154     Ile Gln Asn Phe Gln Lys Gly Thr Leu Arg Lys Ala Lys
155     555               560               565
156     acc tgt gat cac agt gct ccg aag atc ggc tg aa 1800
157     Thr Cys Asp His Ser Ala Pro Lys Ile Gly
158                570               575       577
159     gcttcctgtt tacacttgga gggaaaagtt cttttttatt cctactcacc 1850
160     cctacccccc aaactaccct cttcctggga aagtaattgc tgagccagta 1900
161     cagccacaaa cagtactatt ttgcagatgc tcatgtaagc agcttttcga 1950
162     gagaaataat tctttaagca gaataaagtt aggctggcat tgctccctta 2000
163     agatcttgct cctttattaa ccctgtaaag gagtcttgtt tatcctctaa 2050
164     tggccaggct tttgggacag cagcatattg aaatattttc accaactaaa 2100
165     ggaaatagac agaaaaacaa tgacaatatt caatcacagc agtaaatggc 2150
166     ctttgtgttg caatcccttc taccccatca gacagctcct agaaacattc 2200
167     cttacagttc atttctctaa agcattttct gattcttaga taactccaat 2250
168     ttttgctacc tttatcttag acattaacac tatagcccaa agcatagtta 2300
169     ctttgctaaa tcagaaagca actgagttct ttgttttctc ctcaaataga 2350
170     atggggaacg ttcacaacat tctcttaagt tctaacagga ataccattgt 2400
171     ggttatagaa ctcagggctg ctaaagcaac tactctagac ccatagttct 2450
172     ttttagttag atgtattgaa acagacaaaa atattaacat cagaaaaagc 2500
173     tcttgccaat tagaggatct tcttaatcct cagcaattaa gtttgggggtt 2550
174     tgaggggggc aggtcattgt tacaacagaa gtaaatttgg catctataga 2600
175     aatcaattat gatttttgaa agatttatct aaatatatca atatagcatc 2650
176     tctttaatgt tagtcalttta ttagaaagat cctttatcct gatttgctta 2700
177     aacctttcaa taaattgcac tttaaaggat tataaataat ccatttaaaa 2750
178     attcaagtac acacatcagt gttggttact atgcagagaa tgtcattgtg 2800
179     tatagtttca tgtaatctgt tatgtcagct gtattttta ttaaaatcat 2850
180     gtcaagaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaa a 2891
182 <210> SEQ ID NO: 2
183 <211> LENGTH: 577
184 <212> TYPE: PRT
185 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 2
187     Met Ala Phe Met Glu Lys Pro Pro Ala Gly Lys Val Leu Leu Asp
188      1               5               10                  15
189     Asp Thr Val Pro Leu Thr Ala Ala Ile Glu Ala Ser Gln Ser Leu
190                    20               25                  30
191     Gln Ser His Thr Glu Tyr Ile Ile Arg Val Gln Arg Gly Ile Ser
192                    35               40                  45
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Input Set : N:\Crf3\RULE60\10811080.raw.txt
Output.Set: N:\CRF4\10182004\J811080.raw

```
193    Val Glu Asn Ser Trp Gln Ile Val Arg Arg Tyr Ser Asp Phe Asp
194                    50                  55                  60
195    Leu Leu Asn Asn Ser Leu Gln Ile Ala Gly Leu Ser Leu Pro Leu
196                    65                  70                  75
197    Pro Pro Lys Lys Leu Ile Gly Asn Met Asp Arg Glu Phe Ile Ala
198                    80                  85                  90
199    Glu Arg Gln Lys Gly Leu Gln Asn Tyr Leu Asn Val Ile Thr Thr
200                    95                  100                 105
201    Asn His Ile Leu Ser Asn Cys Glu Leu Val Lys Lys Phe Leu Asp
202                    110                 115                 120
203    Pro Asn Asn Tyr Ser Ala Asn Tyr Thr Glu Ile Ala Leu Gln Gln
204                    125                 130                 135
205    Val Ser Met Phe Phe Arg Ser Glu Pro Lys Trp Glu Val Val Glu
206                    140                 145                 150
207    Pro Leu Lys Asp Ile Gly Trp Arg Ile Arg Lys Lys Tyr Phe Leu
208                    155                 160                 165
209    Met Lys Ile Lys Asn Gln Pro Lys Glu Arg Leu Val Leu Ser Trp
210                    170                 175                 180
211    Ala Asp Leu Gly Pro Asp Lys Tyr Leu Ser Asp Lys Asp Phe Gln
212                    185                 190                 195
213    Cys Leu Ile Lys Leu Leu Pro Ser Cys Leu His Pro Tyr Ile Tyr
214                    200                 205                 210
215    Arg Val Thr Phe Ala Thr Ala Asn Glu Ser Ser Ala Leu Leu Ile
216                    215                 220                 225
217    Arg Met Phe Asn Glu Lys Gly Thr Leu Lys Asp Leu Ile Tyr Lys
218                    230                 235                 240
219    Ala Lys Pro Lys Asp Pro Phe Leu Lys Lys Tyr Cys Asn Pro Lys
220                    245                 250                 255
221    Lys Ile Gln Gly Leu Glu Leu Gln Gln Ile Lys Thr Tyr Gly Arg
222                    260                 265                 270
223    Gln Ile Leu Glu Val Leu Lys Phe Leu His Asp Lys Gly Phe Pro
224                    275                 280                 285
225    Tyr Gly His Leu His Ala Ser Asn Val Met Leu Asp Gly Asp Thr
226                    290                 295                 300
227    Cys Arg Leu Leu Asp Leu Glu Asn Ser Leu Leu Gly Leu Pro Ser
228                    305                 310                 315
229    Phe Tyr Arg Ser Tyr Phe Ser Gln Phe Arg Lys Ile Asn Thr Leu
230                    320                 325                 330
231    Glu Ser Val Asp Val His Cys Phe Gly His Leu Leu Tyr Glu Met
232                    335                 340                 345
233    Thr Tyr Gly Arg Pro Pro Asp Ser Val Pro Val Asp Ser Phe Pro
234                    350                 355                 360
235    Pro Ala Pro Ser Met Ala Val Val Ala Val Leu Glu Ser Thr Leu
236                    365                 370                 375
237    Ser Cys Glu Ala Cys Lys Asn Gly Met Pro Thr Ile Ser Arg Leu
238                    380                 385                 390
239    Leu Gln Met Pro Leu Phe Ser Asp Val Leu Leu Thr Thr Ser Glu
240                    395                 400                 405
241    Lys Pro Gln Phe Lys Ile Pro Thr Lys Leu Lys Glu Ala Leu Arg
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 10/18/2004
PATENT APPLICATION: US/10/811,080   TIME: 10:03:40

Input Set : **N:\Crf3\RULE60\10811080.raw.txt**
Output Set: **N:\CRF4\10182004\J811080.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 162,165,183,184,187,204,207,211,216,219,222,223,225,237,240
Seq#:5; N Pos. 244,250,253,262,267,269,275,279,282,289,290
Seq#:9; N Pos. 379,433,459,492,517,541,549,561,575,579,582,710,742,774,784
Seq#:13; N Pos. 103
Seq#:13; Xaa Pos. 11
Seq#:15; N Pos. 74,1306
Seq#:16; Xaa Pos. 104
Seq#:17; N Pos. 4,107,109,112,119,122,176,323,1616,1878,1881,1911,1924,1939
Seq#:17; N Pos. 1953,1982,1991,1992,2000,2443
Seq#:17; Xaa Pos. 18,449
Seq#:18; Xaa Pos. 18,448
Seq#:19; N Pos. 300

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:9; Line(s) 511

VERIFICATION SUMMARY   DATE: 10/18/2004
PATENT APPLICATION: **US/10/811,080**   TIME: 10:03:40

    Input Set : **N:\Crf3\RULE60\10811080.raw.txt**
    Output Set: **N:\CRF4\10182004\J811080.raw**

```
L:479 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:150
M:341 Repeated in SeqNo=5
L:521 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:350
M:341 Repeated in SeqNo=9
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:91
M:341 Repeated in SeqNo=13
L:830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:50
M:341 Repeated in SeqNo=15
L:938 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:90
L:982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:15
M:341 Repeated in SeqNo=18
L:1225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:250
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